

Maximum Likelihood

(106 gene sequences, 80027 aligned nucleotide bases)

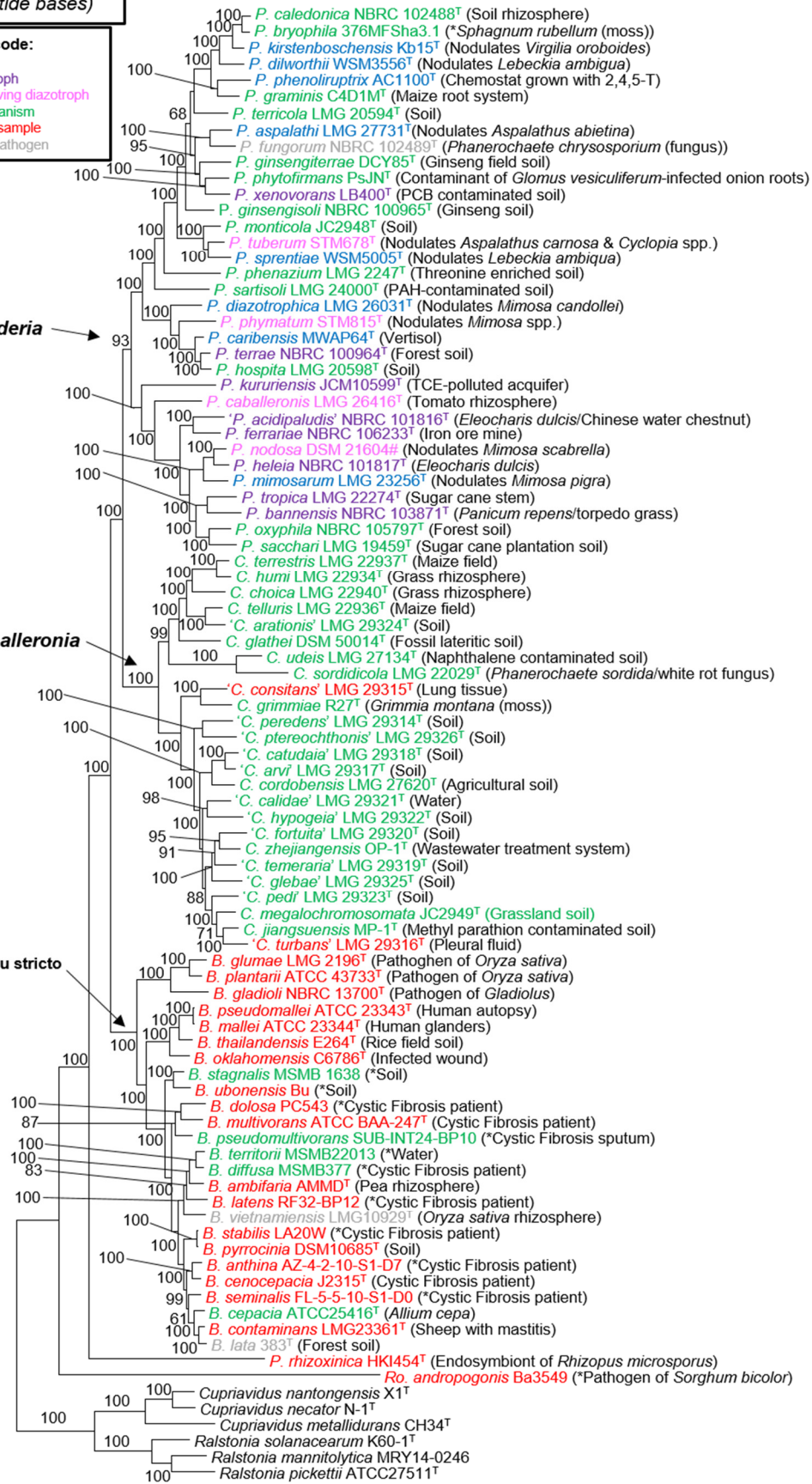
Species colour code:

- Nodulator
- Free-living diazotroph
- Nodulator + free-living diazotroph
- Environmental organism
- Pathogen/Clinical sample
- Environmental + Pathogen

Paraburkholderia

Caballeronia

Burkholderia sensu stricto



0.05

Supplementary Figure S3. Maximum-likelihood phylogeny of the nucleotide sequences of 106 conserved genes for the 92 strains investigated in this study. The partitioned dataset employed independent model parameter estimates for the General Time Reversible model (GTR; Tavaré, 1986) for each partition and was analysed in RAxML v 8.2 (Stamatakis, 2014). Values indicated at nodes were inferred for 1000 bootstrap pseudo-replicate datasets.